

Input file F1h14273new; Output File F1h14273tra  
Sequence length 1743

G	D	A	P	L	R	S	L	E	Q	A	N	R	T	P	F	F	C	A	R	A	A	9
GGC	GAC	GCG	CCC	TTG	CGC	AGC	CTG	GAG	CAA	GCC	AAC	CGC	ACC	CCC	TTT	CCC	TTC	TTC	TCC	TCC	27	
D	V	K	G	D	H	R	L	V	L	A	A	V	E	T	T	V	L	V	L	V	29	
GAC	GTC	AAG	GGC	GAC	CAC	CGG	CTG	GTG	CTG	GCC	GGC	GTG	GAG	ACA	ACC	GTG	CTG	GTG	CTG	147		
I	F	A	V	S	L	G	N	V	C	A	L	V	L	V	A	R	R	R	R	49		
ATC	TTT	GCA	GTC	GTG	TCG	CTG	CTG	GGC	AAC	GTG	TGC	GCC	CTG	GTG	CTG	GTG	CTG	GTG	CGA	CGA	207	
R	R	G	A	T	A	C	L	V	L	N	L	F	C	A	D	L	L	F	I	69		
GGC	CGC	GGC	GGC	ACT	GCC	TGC	CTG	GTA	CTC	AAC	CTC	TTC	TGC	GCG	GAC	CTG	CTG	CTC	TTC	ATC	267	
S	A	I	P	L	V	L	A	V	R	W	T	E	A	W	L	L	G	P	V	109		
AGC	GCT	ATC	CCT	CTG	GTG	CTG	GCC	GTG	CGC	TGG	ACT	GAG	GCC	TGG	CTG	GGC	CCC	GTT	327			
A	C	H	L	L	F	Y	V	M	T	L	S	G	S	V	T	I	L	T	L	129		
GCC	TGC	CAC	CTG	CTG	CTC	TTC	TAC	GTG	ATG	ACC	CTG	AGC	GGC	AGC	GTC	ACC	ATC	CTC	ACG	CTG	387	
A	A	V	S	L	E	R	M	V	C	I	V	H	L	Q	R	G	V	R	G	147		
GCC	GCG	GTC	AGC	CTG	GAG	CGC	ATG	GTG	TGC	ATC	GRG	CAC	CTG	CAG	CGC	GGC	GTG	CGG	GGT	447		
P	G	R	R	A	R	A	V	L	L	A	L	I	W	G	Y	S	A	V	A	169		
CCT	CGG	CGG	CGG	CGG	CGG	GCA	GTC	CTG	CTG	GCG	CTC	ATC	TGG	GCC	TAT	TCG	GCG	GTC	GCC	507		
A	L	P	L	C	V	F	F	R	V	V	P	Q	R	L	P	G	A	D	Q	189		
GCT	CTG	CCT	CTG	CTC	TGC	GTC	TTC	TTT	CGA	GTC	CCG	CAA	CGG	CTC	CCC	GGC	GAC	GAC	CAG	567		

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TO FIG. 1B.

**FIG. 1A.**



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FROM FIG. 1A.

E	I	S	I	C	T	L	I	W	P	T	I	G	E	I	S	W	D	V	209	
GAA	ATT	TCG	ATT	TGC	ACA	CTG	ATT	TGG	CCC	ACC	ATT	CCT	GGG	GAG	ATC	TCG	TGG	GAT	GTC	627
S	F	V	T	L	N	F	L	V	P	G	L	V	I	V	I	S	Y	S	K	229
TCT	TTT	GTT	ACT	TTG	AAC	TTC	TTG	GTC	CCA	GGG	CTG	GTC	ATT	GTG	ATC	AGT	TAC	TCC	AAA	687
I	L	Q	I	T	K	A	S	R	K	R	L	T	V	S	L	A	Y	S	E	249
ATT	TTA	CAG	ATC	ACA	AAG	GCA	TCA	AGG	AAG	AGG	CTC	ACC	GTA	AGC	CTG	GCC	TAC	TCG	GAG	747
S	H	Q	I	R	V	S	Q	Q	D	F	R	L	F	R	T	L	F	L	L	269
AGC	CAC	CAG	ATC	CGC	GTG	TCC	CAG	CAG	GAC	TTC	CGG	CTC	TTC	CGC	ACC	CTC	TTC	CTC	CTC	807
M	V	S	F	I	M	W	S	P	I	I	T	I	L	L	I	L	I	L	I	208
ATG	GTC	TCC	TTC	TTC	ATC	ATG	TGG	AGC	CCC	ATC	ATC	ATC	ACC	ATC	CTC	CTC	ATC	CTG	ATC	867
Q	N	F	K	Q	D	L	V	I	W	P	S	L	F	F	W	V	V	A	F	309
CAG	AAC	TTC	AAG	CAA	GAC	CTG	GTC	ATC	TGG	CCG	TCC	CTC	TTC	TTC	TGG	GTC	GCC	GCC	TTC	927

TO FIG. 1C.

**FIG. 1B.**



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FROM FIG. 1B.

T	F	A	N	S	A	L	N	P	I	L	Y	N	M	T	L	C	R	N	E
ACA	TTT	GCT	AAT	TCA	GCC	CTA	AAC	CCC	ATC	CTC	TAC	AAC	ATG	ACA	CTG	TGC	AGG	AAT	GAG
W	K	K	I	F	C	C	F	W	F	P	E	K	G	A	I	L	T	D	T
TGG	AAG	AAA	ATT	TTT	TGC	TGC	TTC	TGG	TTC	CCA	GAA	AAG	GGA	GCC	ATT	TTA	ACA	GAC	ACA
S	V	K	R	N	D	L	S	I	I	S	G	•	362						1047
TCT	GTC	AAA	AGA	AAT	GAC	TTC	TGC	ATT	ATT	TCT	GGC	TAA	1086						

TTTTCTTATAAGCGAGTTCTCACACCTGGCGAGCTGTGGCATGCTTTAAACAGAGTTCATTTCCAGTACCCCTCCA  
 TCAGTGACCCCTGCTTAAGAAAATGAACCTATGCAAATAGACATCCACAGGGTCGGTAAATTAGGGGTGATCACCAA  
 GTTTCATTAATTTCCCTTATAAAAGGATTGTTGGCCAGGTGCAGTGTTCATGCCTGTAATCCCAGCAGTTGGG  
 AGGCTGAGGTGGTGGATCACCTGAGGTCAAGGAGTTCGAGAACCAACCTGACCAACATGGTGAGACCCCCGGTCTACTA  
 AAAATAAAAAAAATTAGCTGGGAGTGGTGGCACCTGTAATCCTAGGTACTGGGAGGCTGAACCAGGAGAAT  
 CTCTTGAAACCTGGGAGGCAAGGTTGCAGTGAGCCAGATCGTGCACCTCCAAACCAAGAGTGAAAC  
 TCCATCTTAAAGGGTTCTTTAAATGTGAACTTTAGTGTGTAAATATG  
 ATCAAATTAAATATTATGACTGTTCAAGCAAAAAAAAGGGGG

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FIG. 1C.



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Sequence	Description	score	E-value	N
7tm_1	<u>PF00001</u> 7 transmembrane receptor (rhodopsin)	119.9	4.7e-37	1

Parsed for domains:

Sequence	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value	-
7tm_1	1/1	57	321	1	259	[ ]	119.9	4.7e-37

Alignments of top-scoring domains:

7tm\_1: domain 1 of 1, from 57 to 321: score 119.9, E = 4.7e-37

\*->GN1LVi1vi1rtkk1rtpnif1NLAVADLLf11t1ppwaiyy1vg  
GN+ ++++++tr ++tr +t +++1NL ADLLF + p++ ++ -+

F1h14273, 57 GNVCALVLVAR-RRRRGATACLVNLFCADLLFISAIPVLVLAVR-WT 101

gaadWpfGsa1Ck1vtaldvvnmyaS11Lta1S1DRY1A1vhP1ryrrr  
e W++G++ C++ +++++++ + i1+L+a S++R + Iv 1+ +r

F1h14373, 102 --EAWLLGPVACHLLFYMTLSGSVTILTAAVSLERMVCIV-HLQRGVR 148

rtsprrrAkvv11vwv1a111s1Pp11fswvktveegngt1nvnnevC1i  
+tr +v+++1+W +++++1P +f+ v+ ++ ++ ++ +C++

F1h14273, 149 GPGRRARAVLLALIWGYSAVAALPLCVFFRVPQRLPG--ADQEISICTL 196

dfpccstasvstw1rsyv11st1wgF11P11vi1vcYtrI1rt1r....  
+p++++ + +s+ +++ ++ F1+P 1vi++ Y+ II + + +++

F1h14273, 197 IWPTRIPG--EISW&VSFTLNELVRGLVIVJSYSKILQITKasrkr 240  
(Note: Dashes indicate gaps in sequence alignment.)

.....kaakt11vvvvvFv1CW1Pyfiv111dt1c  
+ + +++++ + + + + +t1+++v F++ W P i++11 +

F1h14273, 241 1cvslayseehqirvsqqdfRLFRTLFLLMVSFFIMWSPIIITILLILIQ 290

.1siimsstCe1erv1pta11vt1wLayvNsc1NPi1Y<-\*  
-- + + + p + + + + +Na+1NPi+Y

F1h14273, 291 nFK-----QDLVIWPSLFWVVAPTFANSALNPILY 321

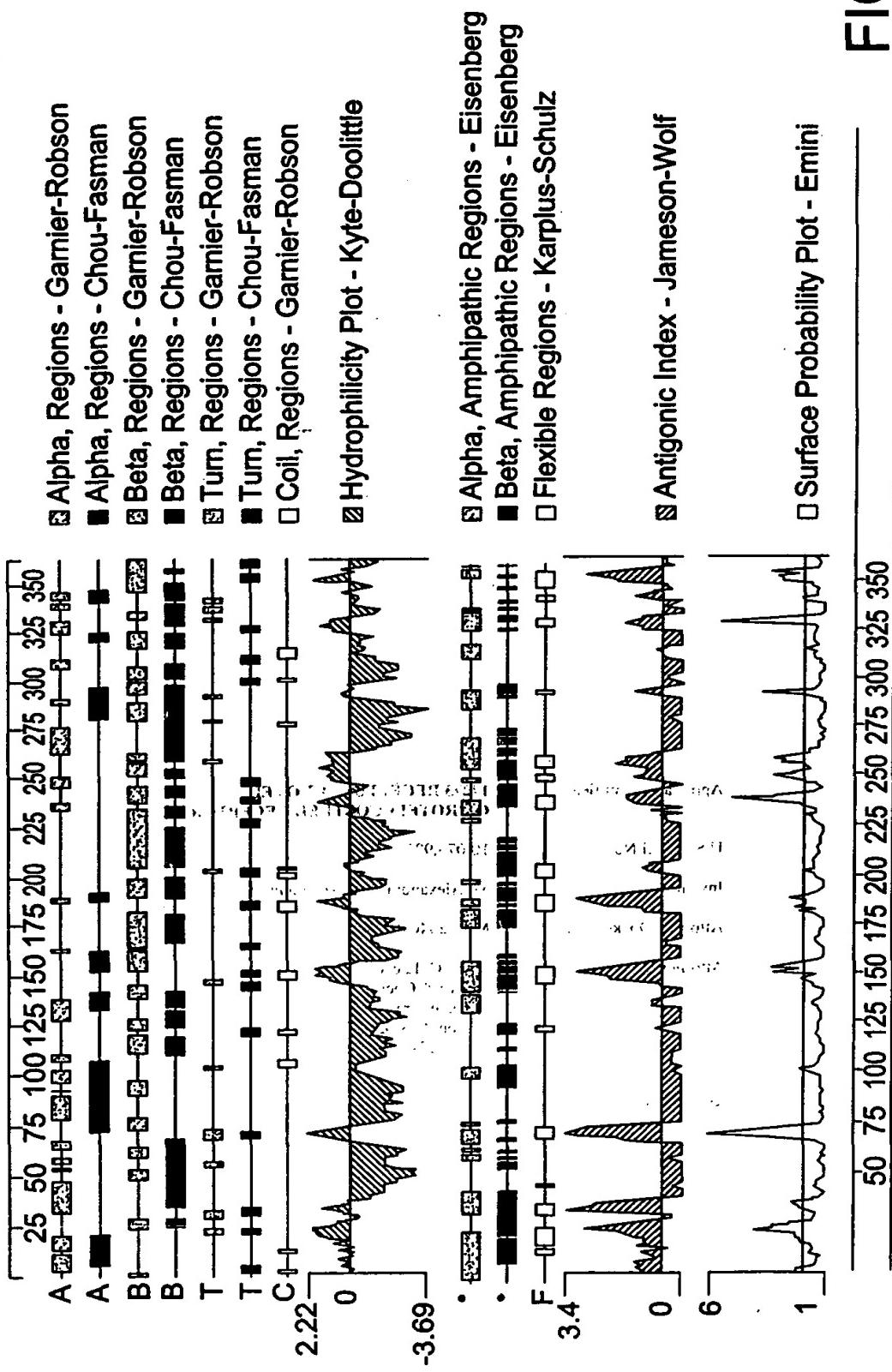
**FIG. 2.**

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A circular logo for OIPE (Oficina de la Propiedad Industrial de Paraguay). The word "OIPE" is at the top, "SCHENK" is on the right, and "PATENT & TRADEMARK OFFICE" is at the bottom.



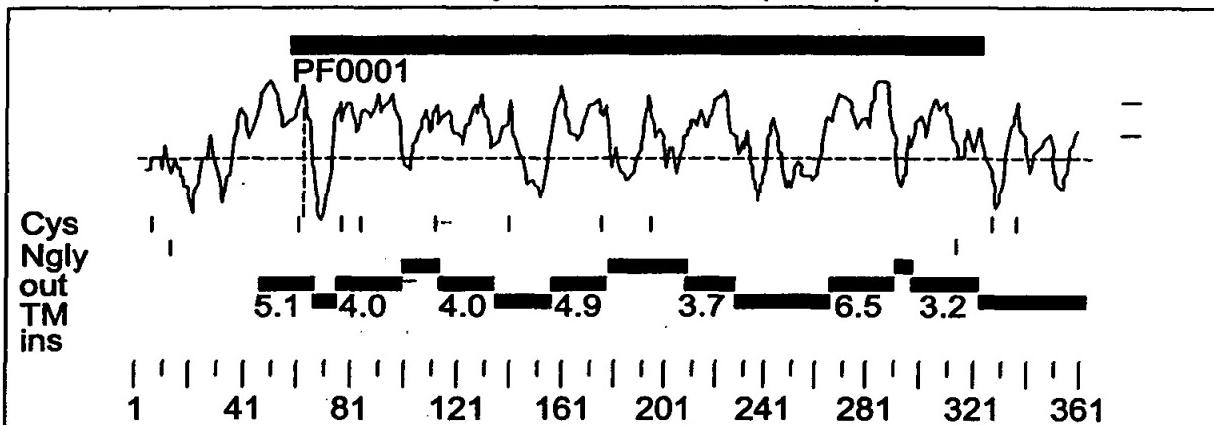


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## Analysis of F1h14273, (362 aa)



>F1h14273, 1086 bases, 1825 checksum.  
MSPECARAQQDAPLRSLEQANRTRFPFFSDVKGDHRLVLAAVETTVLVLEFAVSLLGNVC  
ALVLVARRRRRGATAQLVNLFCADLLFYSAIPLVLA VRWTEAVLLGPVACHLLFYVMTL  
SGSVTILTAAVSLERMVCIVHLQRCVRGPGRARAVLLAIWGYSAVAALPLCVFFRVV  
PQRLPGADQEISICTLIWPTIPGEISWDSFVTLNLFVYPGLVIVISYSKILQITKASRKR  
LTVSLAYSESHQIRVSQQDFRLFRTLFLMVSFFIMWSPIIITILLILIQNFKQDLVIWP  
SLFFFVVVAFTFANSALNPILYNMTLCRNEWKKIFCCPWFGPEKGAILTDTSVKRNDSIIS  
G+

FIG. 4.



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Prosite Pattern Matches for F1h14273

>PS00001/PDOC00001/ASN\_GLYCOSYLATION N-glycosylation site.

Query: 21 NRTR 24

Query: 322 NMTL 325

>PS00004/PDOC00004/CAMP\_PHOSPHO\_SITE cAMP- and cGMP-dependent protein kinase phosphorylation

Query: 239 KRLT 242

>PS00005/PDOC00005/PKC\_PHOSPHO\_SITE Protein kinase C phosphorylation site.

Query: 237 SRK 239

Query: 350 SVK 352

>PS00006/PDOC00006/GK2\_PHOSPHO\_SITE Casein kinase II phosphorylation site.

Query: 256 SQQD 259

>PS00008/PDOC00008/MYRISTYL N-myristylation site.

Query: 57 GNVCAL 62

Query: 72 GATACL 77

Query: 343 GAILTD 348

>PS00009/PDOC00009/AMIDATION Amidation site.

Query: 150 PCRR 153

>PS00029/PDOC00029/LEUCINE\_ZIPPER Leucine zipper pattern.

Query: 106 LGPVACHLLFYVMTLSGSVTIL 127

FIG. 5.



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## Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
46	66	out->ins	5.1
75	98	ins->out	4.0
113	134	out->ins	4.0
156	177	ins->out	4.9
209	227	out->ins	3.7
266	289	ins->out	6.5
297	321	out->ins	3.2

>F1h14273,  
MSPECARAAGDAPLRSLEQANRTRFPFFSDVKGDHRLVLAAVETTVLVIIPAVSLLGNVC  
ALVLVARRRRRGATACLVNLFCADLLFISAWPLVLAVRWTEAWLLGPVACHLLFYVMTL  
SGSVTILTAAVSLERMVCIVHLQRGVRGPGRARRAVALLAIWGYSAVAALPLCVFFRVV  
PQLPGADQEISICTLIWPTIPGEISWDVSFVTLNFLVPGLVIVISYSKILQITKASRKR  
LTVELAYSESHQIRVSQQDFRLFRTLFLMVSFFIMWSPIIITILLILIQNFKQDLVIWP  
SLFFFVVVAFTFANSALNPILYNMTLCRNEWKKIPCCFWFPEKGAILTDTSVKRNDLSIIS  
G

## Transmembrane Segments for Presumed Mature Peptide

Start	End	Orient	Score
14	37	ins->out	4.0
52	73	out->ins	4.0
95	116	ins->out	4.9
148	166	out->ins	3.7
205	228	ins->out	6.5
236	260	out->ins	3.2

>F1h14273,\_mature  
LVLVARRRRRGATACLVNLFCADLLFISAIPLVLAVRWTEAWLLGPVACHLLPYVMTLS  
GSVTILTAAVSLERMVCIVHLQRGVRGPGRARRAVALLAIWGYSAVAALPLCVFFRVV  
PQLPGADQEISICTLIWPTIPGEISWDVSFVTLNFLVPGLVIVISYSKILQITKASRKR  
TVELAYSESHQIRVSQQDFRLFRTLFLMVSFFIMWSPIIITILLILIQNFKQDLVIWPS  
LFFFVVVAFTFANSALNPILYNMTLCRNEWKKIPCCFWFPEKGAILTDTSVKRNDLSIISG

**FIG. 6.**



Input file 14273m; Output File 14273mtra  
Sequence length 1560  
TTGCCAAGCTCAGGGTAAGCCTCTTCCACTCACAGAAGGTTCATGGAGTGCTTCACACCATCAGTGACCA

	M	S	P	E	C	A	Q	T	T	G	10										
P	G	P	S	H	T	L	D	Q	V	N	R	T	H	F	P	F	S	D	30		
CCT	GCT	CCC	TCG	CAC	ACC	CTG	GAC	CGA	AA	GTC	AAT	CCG	ACC	CAC	TTC	CCT	TTC	TTC	TG	GAT	90
V	K	G	D	H	R	L	V	E	S	V	E	T	T	V	L	G	L	I	1	50	
GTC	AAG	GGC	GAC	CAC	CGG	TTC	GTC	GTC	GTC	GAG	ACC	ACC	GTC	GTC	GTC	GTC	GTC	GTC	ATC	150	
F	V	V	S	L	L	V	N	C	A	L	V	L	V	A	R	R	R	R	70		
TTT	GTC	GTC	TCA	C TG	CTG	TTC	GTC	TGT	GCT	CTA	GTC	CTG	GTC	210							
R	G	A	S	A	S	N	L	V	L	N	L	F	C	A	D	L	L	F	T	90	
CGT	GGG	GCG	TCA	GCC	AGC	CTG	GTG	CTC	AAC	CTC	TTC	TGC	GCG	GAT	TTG	CTC	TTG	CTC	TTG	AGC	270
A	I	P	L	V	L	V	R	W	T	E	A	W	L	L	G	P	V	V	V	110	
GCC	ATC	CCT	CTA	GTG	CTC	GTC	GTG	CGC	TGG	ACT	GAG	GCC	TGG	CTG	TTG	GGG	CCC	GTC	GTC	330	
C	H	L	L	F	Y	V	M	T	M	S	G	S	V	T	I	L	T	L	A	130	
TGC	CAC	CTG	CTC	TTC	TAC	GTG	ATG	ACA	ATG	AGC	AGC	GTC	AGC	ATC	CTC	ACA	CTG	GCC	390		
A	V	S	L	E	R	M	V	C	I	V	R	L	R	R	G	L	S	G	P	150	
GCG	GTC	AGC	CTG	GAG	CGC	ATG	GTG	TGC	ATC	GTG	CGC	CTC	CGG	CGC	GGC	TTG	AGC	GGC	CCG	450	
G	R	R	T	Q	A	A	L	L	A	F	I	W	G	Y	S	A	L	A	A	170	
GGG	CGG	CGG	ACT	CAG	GCG	GCG	GCA	CTG	CTG	GCT	TTC	ATA	TGG	GGT	TAC	TGG	GCG	CTC	GCG	510	

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TO FIG. 7B.

FIG. 7A.



FROM FIG. 7A.

C	TG	CCC	C	TAC	TAC	TTC	TTG	GGC	GTC	GTC	CGC	CAG	CGC	CTT	CCC	GGC	G	D	Q	E	
I	P	I	C	T	L	D	W	P	N	R	I	G	E	I	S	W	D	V	F	210	
F	E	T	L	N	F	L	V	P	G	L	V	I	V	I	S	Y	S	K	I	230	
L	Q	I	T	K	A	S	R	K	R	L	T	L	S	L	A	Y	S	E	S	250	
H	Q	I	R	V	S	Q	Q	D	Y	R	L	F	R	T	L	F	L	L	M	270	
CAC	CAG	ATC	CGA	GTG	TCC	CAA	CAA	GAC	TAC	CGA	CTC	TTC	CGC	AGC	CTC	TTC	CTG	CTG	CTG	ATC	810
V	S	F	F	I	M	W	S	R	I	I	T	I	L	L	I	L	I	Q	290		
GTT	TCC	TTC	TTC	ATC	ATG	TGG	AGT	TCC	ATC	ATC	ACC	ATC	CTC	CTC	ATC	ATC	ATC	ATC	CAA	870	
N	F	R	Q	D	L	V	I	P	S	L	F	F	W	V	V	A	F	T	310		
AAC	TTC	CGG	CAG	GAC	CTG	GTC	ATC	TGG	CCA	TCC	CTT	TTC	TTC	TGG	GTC	GTC	GCC	TTC	ACG	930	
F	A	N	S	A	L	N	P	I	L	Y	N	M	S	L	F	R	N	E	W	330	
TTT	GCC	AAC	TCT	GCC	CTA	AAC	CCC	ATA	CTG	TAC	AAC	ATG	TGG	CTG	CTG	TTC	AGG	AGC	GAA	TGG	990
R	K	I	F	C	C	F	F	P	E	K	G	A	I	F	T	D	T	S	350		
AGG	AAG	ATT	TTT	TGC	TTC	TTT	TTT	CCA	GAG	AAG	GGA	GCC	ATT	TTT	ACA	GAT	ACG	TCT	1050		
V	R	R	N	D	L	S	V	I	S	S	•								362		
GTC	AGG	CGA	AAT	GAC	TTG	TCT	GTT	ATT	TCC	AGC	TAA								1088		

CTAGCCCTCTGGTGCCAGGTGAACACACGGTTAAGCGAGTTAACCTCAAGGAAGCCACCGAGTGGCCCTGC  
TTTAAAAATAACCCGACTTCCAAACAGCAGGCATCTACGGAGCCAGCAATTAAAGGAATGATCGCTCAGTATAAAATATT  
TTTCCTTAAGAACACTTTCTATGGTTCCCTTTGTGAACTTTTTAAGTGTGTTAATATGATCTAGTTAATAAAATT  
TTTATTATAACGTGTCTCCTACAAAAAAA

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FIG. 7B.

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Query: 14273m,

Scores for sequence family classification (score includes all domains):

<u>Sequence</u>	<u>Description</u>		<u>Score</u>	<u>E-value</u>	<u>N</u>
7tm_1	PF00001	7 transmembrane receptor (rhodopsin)	118.8	1e-35	1

Parsed for domains:

Sequence	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
7tm_1	1/1	57	321 ..	1	259 [ ]	118.8	1e-36

## Alignments of top-scoring domains:

7tm\_1: domain 1 of 1, from 57 to 321: score 118.8, E = 1e-36  
\*->GN1LVi1v1lrtkk1rtptnif1NLAvADLLf11t1ppwaiyy1vg

14273m, 57 GNV CAL VL VAR-RRRRGASASLVLNLFCADLLFTSAIPLVLVVR-WT 101

gaadWpfGaa1Ck1vta1dvvnmyaSi111Lta1S;DRY1A1vhP1ryrrr  
e W++G+++C+1+ +++++++ + 11+L+a S++R + Iv 1r +

14273m, 102 --EAWLLGPVVCHLLPYVMTMSGSVTILTAAVSLERMVCIV-RLRRGLS 148

rtsprA.kvv*i*11vW*v*1a111s1P*p*11f*s*w*v*k*t*v*e*a*g*n*g*t*1**nv**n**v**t**v*C1  
r+r+t+t+t+t+W++t+t+1P+++++v++t++t+t+t+f+t+

14273m. 149 GP-GRRT QAAALLAFIWGYSALAALPLYIILFRVVVPQRLLPGGD--QEITPCT 195

idfppeestasvstw1rsyv11st1vgF21P11v1voYtr11rt1r...  
tdtptt + t+st ttt tt F1tP 1vitt Yt 11 t + ttt

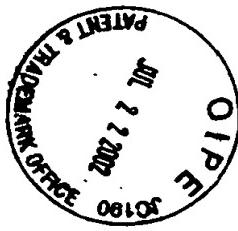
14273m. 196 | DWPNRIG-----EISWDVEETLNEIVPGIVIVISYSKILQITKosrk 239

14273m, 240 r1t1s1aysesthqirvssqqdyRLFRTLFLLMVSFFIMWSPIIITILLILI 289

c. laiimestCelerv1ptailvt1wLayvNsc1NPi1Y<-\*  
++ + + p +++++ + +++++Ns+1NPi+Y

14273m, 290 QnFR-----QDLVIWPSLFFWWVVAFTFANSALNPILY 321

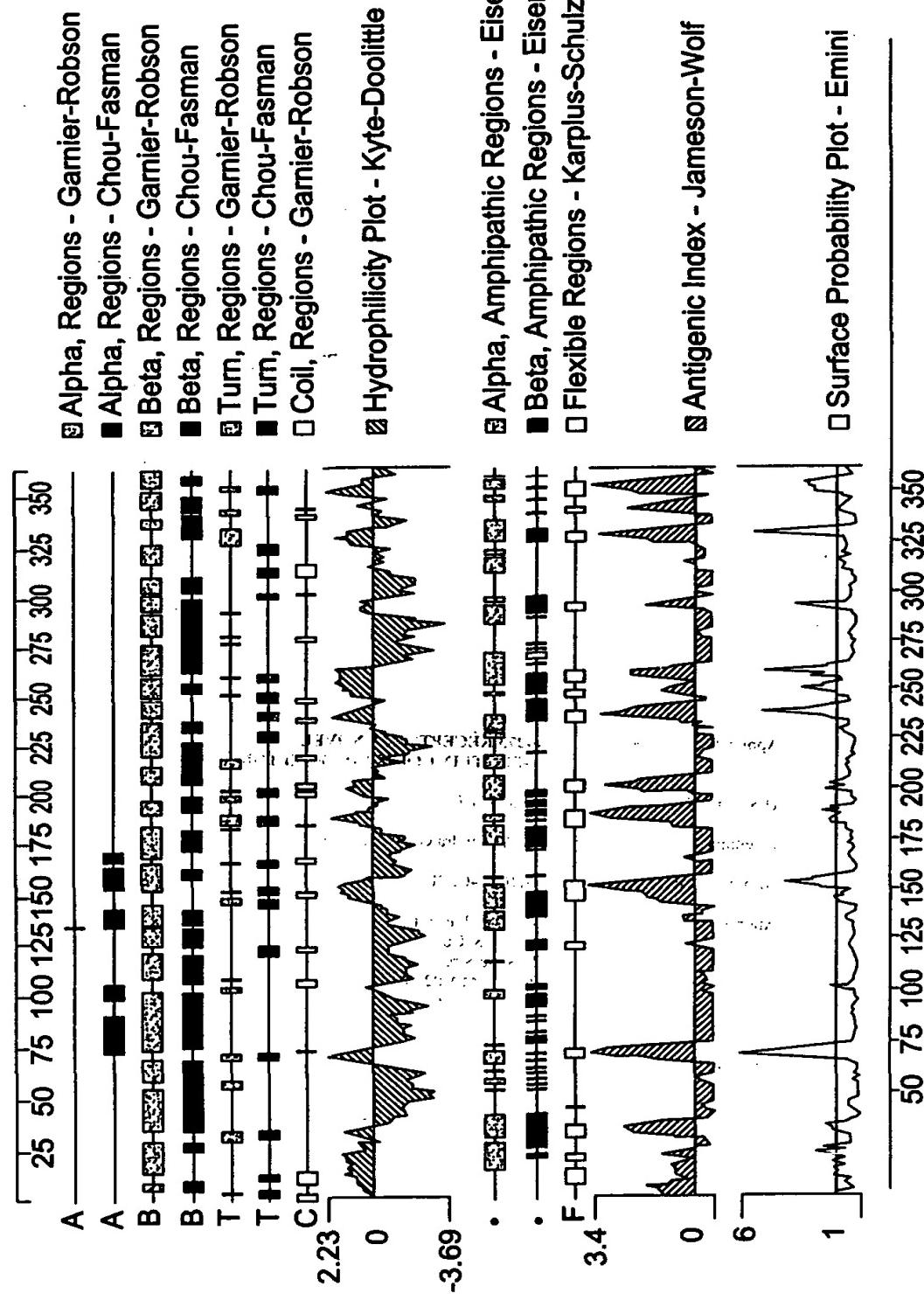
## FIG. 8.



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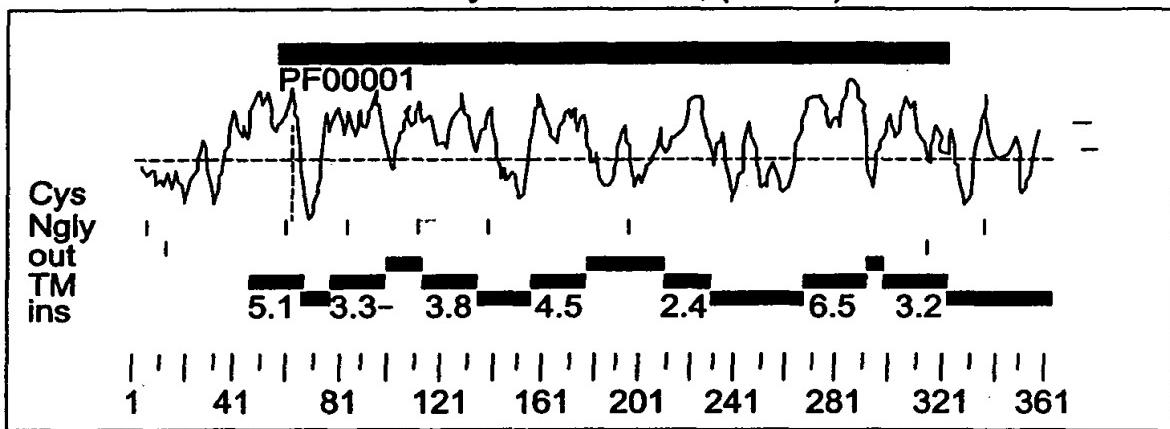
**FIG. 9.**



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## Analysis of 14273m, (362 aa)



>14273m, 1086 bases, 6943 checksum.  
 MSPECACQTTGCPSPHTLDQVNRTHFPPFSDVKGDHRLVLSVVETTVLGLIFVVSLLGNVC  
 ALVLVARRRRRGASASLVNLFCADLLFTSAIPLVLLVVRWTEAWLLGPVVCHLLFVVMTM  
 SGSVTILTAAVSLERMVCIVRLRRGLSGPGRRTQAALLAFIWGYSALAALPLYILFRVV  
 PQRLPGGDQEIPICTLDWPNRIGEISWDVFFETLNFLVPGLVIVVISYSKILQITKASRKR  
 LTLSLAYSESHQIRVSQQDYRLFRTLFLLMVSSFIWSRIIITILLILIQNFRQDLVIWP  
 SLFFFVVVAFTFANSALNPILYNMSLFRNEWRKIFCCFPFPEKGAIFTDTSVRRNDSLVIS  
 S\*

**FIG. 10.**



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## Prosite Pattern Matches for 14273m,

>PS00001/PDOC00001; ASN\_GLYCOSYLATION N-glycosylation site.

Query: 21      NRTI    24  
Query: 322     NRTI    325

>PS00002/PDOC00002/GLYCOSAMINOLYCAN Glycosaminoglycan attachment site.

RU      Additional rules:

RU      There must be at least two acidic amino acids (Glu or Asp) from -2 to -4 relative to the serine.

Query: 148     SGPG    151

>PS00004/PDOC00004/CAMP\_PHOSPHO\_SITE cAMP- and cGMP-dependent protein kinase phosphorylation

Query: 239     KRLT    242

>PS00005/PDOC00005/PKC\_PHOSPHO\_SITE Protein kinase C phosphorylation site.

Query: 237     SRK    239  
Query: 350     SVR    352

>PS00006/PDOC00006/CK2\_PHOSPHO\_SITE Casein kinase II phosphorylation site.

Query: 40      SVVE    43  
Query: 256     SQQD    259

>PS00008/PDOC00008/MYRISTYL N-myristoylation site.

Query: 57      GNVCAL 62  
Query: 72      GASASL 77  
Query: 343     GAIFTD 348

>PS00009/PDOC00009/AMIDATION Amidation site.

Query: 150     PGRR    153

**FIG. 11.**



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### Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
46	66	out->ins	5.1
77	98	ins->out	3.3
113	134	out->ins	3.8
156	177	ins->out	4.5
209	227	out->ins	2.4
266	289	ins->out	6.5
297	321	out->ins	3.2

>14273m,  
MSPECAQTTGPGPSHTLDQVNRTHFPPSDVKGDHRLVLSVVETTVLGLIFVVSLLGNVC  
ALVLVARRRRRGASASLVNLFCADLLFTSAIPLVLVVRWTEAWLLGPVVCHLLFYVM  
SGSVTILTAAVSLERMVCIVRLRRLSGPGRRTQAALLAFIWGYSALAALPLYILFRVV  
PQLPQGDQEIPICTLDWPNRIGEISWDVFETLNFLVPGLVIVVISYSKILQITKASRK  
LTLSLAYSESHQIRVSQQDYRLFRTLFLLMVSFFIMWSPIIITILLILIQNFRQDLVIWP  
SLFFWVVAFTFANSALNPILYMMMSLFRNEWRKIFCCFFFPEKGAIFTDTSVRRNDLSVI  
S

### Transmembrane Segments for Presumed Mature Peptide

Start	End	Orient	Score
16	37	ins->out	3.3
52	73	out->ins	3.8
95	116	ins->out	4.5
148	166	out->ins	2.4
205	228	ins->out	6.5
236	260	out->ins	3.2

>14273m, \_mature  
LVLVARRRRRGASASLVNLFCADLLFTSAIPLVLVVRWTEAWLLGPVVCHLLFYVMGMS  
GSVTILTAAVSLERMVCIVRLRRLSGPGRRTQAIIIAFIWGYSALAALPLYILFRVVP  
QRLPQGDQEIPICTLDWPNRIGEISWCVFFETLNFLVPGLVIVVISYSKILQITKASRK  
TLSLAYSESKQIRVSQQDYRLFRTLFLLMVSFTMWSPPIIITILLILIQNFRQDLVIWPS  
LFFWVVAFTFANSALNPILYNMSLFRNEWRKIFCCFFFPEKGAIFTDTSVRRNDLSVISS

**FIG. 12.**